

H8

OIPE

RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/737,476B

TIME: 12:43:23

Input Set : A:\09737476.txt

Output Set: N:\CRF3\08092001\I737476B.raw

ENTERED

4 <110> APPLICANT: Leo G.J. FRENKEN
 5 Cornelis P.E. van der LOGT
 6 Vin-Miin TEH
 7 Martine E. VERHOEYEN
 8 Joy E. WILKINSON
 9 Stephen A. JOBLING
 11 <120> TITLE OF INVENTION: Production of Antibodies
 13 <130> FILE REFERENCE: PNK/060113/0275850 - T7060C
 15 <140> CURRENT APPLICATION NUMBER: US 09/737,476B
 17 <141> CURRENT FILING DATE: 2000-12-18
 19 <150> PRIOR APPLICATION NUMBER: EP 99310188.0
 21 <151> PRIOR FILING DATE: 1999-12-17
 23 <160> NUMBER OF SEQ ID NOS: 67
 25 <170> SOFTWARE: MS Word
 27 <210> SEQ ID NO: 1
 29 <211> LENGTH: 440
 31 <212> TYPE: DNA
 33 <213> ORGANISM: Artificial Sequence ✓
 35 <220> FEATURE:
 37 <223> OTHER INFORMATION: VHH with peptide linker ✓
 39 <220> FEATURE:
 41 <221> NAME/KEY: CDS
 43 <222> LOCATION: (1)..(417)
 45 <400> SEQUENCE: 1
 47 cag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct ggg ggc 48
 48 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 49 1 5 10 15
 51 tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt ggt cat 96
 52 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
 53 20 25 30
 55 ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag gag cgt 144
 56 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
 57 35 40 45
 59 gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg tat aaa 192
 60 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
 61 50 55 60
 63 gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc aag act 240
 64 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
 65 65 70 75 80
 67 acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt 288
 68 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 69 85 90 95
 71 tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg 336
 72 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 73 100 105 110
 75 gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca 384
 76 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser

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77          115          120          125
79 gaa caa aaa ctc atc tca gaa gag gat ctg aat taataagggc taagctcgaa 437
80 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn ✓
81      130          135
83 ttc 440
86 <210> SEQ ID NO: 2
88 <211> LENGTH: 139
90 <212> TYPE: PRT
92 <213> ORGANISM: Artificial Sequence ✓
94 <220> FEATURE:
96 <223> OTHER INFORMATION: VHH with peptide linker ✓
98 <400> SEQUENCE: 2
100 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
101 1          5          10          15
103 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
104      20          25          30
106 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
107      35          40          45
109 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
110      50          55          60
112 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
113 65          70          75          80
115 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
116      85          90          95
118 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
119      100          105          110
121 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
122      115          120          125
124 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn ✓
125      130          135
128 <210> SEQ ID NO: 3
130 <211> LENGTH: 11
132 <212> TYPE: PRT
134 <213> ORGANISM: Artificial Sequence ✓
136 <220> FEATURE:
138 <223> OTHER INFORMATION: myc linker ✓
140 <400> SEQUENCE: 3
142 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
143 1          5          10
146 <210> SEQ ID NO: 4
148 <211> LENGTH: 471
150 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence ✓
154 <220> FEATURE:
156 <223> OTHER INFORMATION: VHH with linker ✓
158 <220> FEATURE:
160 <221> NAME/KEY: CDS
162 <222> LOCATION: (1)..(459)
164 <400> SEQUENCE: 4

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166 cag gtg cag ctg cag cag tca ggg gga ggc ttg gtg cag gct ggg ggg      48
167 Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
168 1          5          10          15
170 tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat      96
171 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
172          20          25          30
174 cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc      144
175 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
176          35          40          45
178 gca act att agt cct ggt ggt agc aca cac tat gta gac tcc gtg aag      192
179 Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
180          50          55          60
182 ggc cga ttc acc atc tcc cga gac aac gcc aag aac aca gtg tat cta      240
183 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
184 65          70          75          80
186 caa atg gac agc ctg aaa cca gag gac acg gcc gtc tat tac tgt gct      288
187 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
188          85          90          95
190 gcc aag ggg agg ggg ctg cag gct atg cag tac tgg ggc cag ggg acc      336
191 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
192          100          105          110
194 ctg gtc acc gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg      384
195 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
196          115          120          125
198 gcc gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc      432
199 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
200          130          135          140
202 tca gaa gag gat ctg aat ggg gcc gca tagtaacaat tg      471
203 Ser Glu Glu Asp Leu Asn Gly Ala Ala
204 145          150
207 <210> SEQ ID NO: 5
209 <211> LENGTH: 153
211 <212> TYPE: PRT
213 <213> ORGANISM: Artificial Sequence ✓
215 <220> FEATURE:
217 <223> OTHER INFORMATION: VHH with linker ✓
219 <400> SEQUENCE: 5
221 Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
222 1          5          10          15
224 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
225          20          25          30
227 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
228          35          40          45
230 Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
231          50          55          60
233 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
234 65          70          75          80
236 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
237          85          90          95

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239 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
240           100           105           110
242 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
243           115           120           125
245 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
246           130           135           140
248 Ser Glu Glu Asp Leu Asn Gly Ala Ala
249 145           150
252 <210> SEQ ID NO: 6
254 <211> LENGTH: 468
256 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence ✓
260 <220> FEATURE:
262 <223> OTHER INFORMATION: VHH with linker ✓
264 <220> FEATURE:
266 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(456)
270 <400> SEQUENCE: 6
272 cag gtg cag ctg cag gag tct ggg gga ggc ctg gtg cag gct ggg ggg      48
273 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
274 1           5           10           15
276 tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata      96
277 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
278           20           25           30
280 gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc      144
281 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
282           35           40           45
284 gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag      192
285 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
286           50           55           60
288 ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg      240
289 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
290 65           70           75           80
292 caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct      288
293 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
294           85           90           95
296 gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg      336
297 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
298           100           105           110
300 gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc      384
301 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
302           115           120           125
304 gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca      432
305 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
306           130           135           140
308 gaa gag gat ctg aat ggg gcc gca tagtaacaat tg      468
309 Glu Glu Asp Leu Asn Gly Ala Ala ✓
310 145           150
313 <210> SEQ ID NO: 7

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RAW SEQUENCE LISTING

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TIME: 12:43:23

Input Set : A:\09737476.txt

Output Set: N:\CRF3\08092001\I737476B.raw

315 <211> LENGTH: 152

317 <212> TYPE: PRT

319 <213> ORGANISM: Artificial Sequence ✓

321 <220> FEATURE:

323 <223> OTHER INFORMATION: VHH with linker ✓

325 <400> SEQUENCE: 7

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328 1 5 10 15
330 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
331 20 25 30
333 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
334 35 40 45
336 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
337 50 55 60
339 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
340 65 70 75 80
342 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
343 85 90 95
345 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
346 100 105 110
348 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
349 115 120 125
351 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
352 130 135 140
354 Glu Glu Asp Leu Asn Gly Ala Ala
355 145 150

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358 <210> SEQ ID NO: 8

360 <211> LENGTH: 462

362 <212> TYPE: DNA

364 <213> ORGANISM: Artificial Sequence ✓

366 <220> FEATURE:

368 <223> OTHER INFORMATION: VHH with linker ✓

370 <220> FEATURE:

372 <221> NAME/KEY: CDS

374 <222> LOCATION: (1)..(450)

376 <400> SEQUENCE: 8

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378 acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48
379 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
380 1 5 10 15
382 gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
383 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
384 20 25 30
386 agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
387 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
388 35 40 45
390 gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
391 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
392 50 55 60
394 gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/737,476B

DATE: 08/09/2001

TIME: 12:43:24

Input Set : A:\09737476.txt

Output Set: N:\CRF3\08092001\I737476B.raw